

OIPE

2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/826,752

DATE: 04/30/2001
TIME: 11:04:49

Input Set : A:\0050.1491-005.TXT
Output Set: N:\CRF3\04302001\I826752.raw

15

ENTERED

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65 Phe Leu Phe Glu Tyr Asn Gln Leu Leu Val Leu Pro Leu Asn Lys Asn	60	65	70	
68 tta ccc tcc ctt aat ttt tca aga aat tcc agt atg aaa tta tcc gct				591
69 Leu Pro Ser Leu Asn Phe Ser Arg Asn Ser Ser Met Lys Leu Ser Ala				
70 75	80	85	90	
72 cta tta gct tta tca gcc tcc acc gcc gtc ttg gcc gct cca gct gtc				639
73 Leu Leu Ala Leu Ser Ala Ser Thr Ala Val Leu Ala Ala Pro Ala Val				
74	95	100	105	
76 cac cat agt gac aac cac cac aac gac aag cgt gcc gtt gtc acc				687
77 His His Ser Asp Asn His His Asn Asp Lys Arg Ala Val Val Thr				
78	110	115	120	
80 gtt act cag tac gtc aac gca gac ggc gct gtt gtt att cca gct gcc				735
81 Val Thr Gln Tyr Val Asn Ala Asp Gly Ala Val Val Ile Pro Ala Ala				
82	125	130	135	
84 acc acc gct acc tcg gcg gct gct gat gga aag gtc gag tct gtt gct				783
85 Thr Thr Ala Thr Ser Ala Ala Asp Gly Lys Val Glu Ser Val Ala				
86	140	145	150	
88 gct gcc acc act act ttg tcc tcg act gcc gcc gct act acc tct				831
89 Ala Ala Thr Thr Leu Ser Ser Thr Ala Ala Ala Ala Thr Thr Ser				
90 155	160	165	170	
92 gcc gcc gcc tct tct tcc tcc tct tcc tcc tcc tct tcc tct tct				879
93 Ala Ala Ala Ser				
94	175	180	185	
96 tcc tct gtt tct ggt gat ttt gaa gat ggt acc att tcc tgt tct				927
97 Ser Ser Val Gly Ser Gly Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser				
98	190	195	200	
100 gat ttc cca tcc gga caa ggt gct gtc tcc ttg gac tgg tta ggt cta				975
101 Asp Phe Pro Ser Gly Gln Gly Ala Val Ser Leu Asp Trp Leu Gly Leu				
102	205	210	215	
104 ggc ggc tgg gct tcc atc atg gac atg aac ggt aac acc gcc acc tct				1023
105 Gly Gly Trp Ala Ser Ile Met Asp Met Asn Gly Asn Thr Ala Thr Ser				
106	220	225	230	
108 tgt caa gac gga tac tac tgt tct tac gct tgt tct cca ggt tac gct				1071
109 Cys Gln Asp Gly Tyr Tyr Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala				
110 235	240	245	250	
112 aag acc caa tgg cct tct gaa caa cct tcc gat ggt aga tcc gtt ggt				1119
113 Lys Thr Gln Trp Pro Ser Glu Gln Pro Ser Asp Gly Arg Ser Val Gly				
114	255	260	265	
116 ggt tta tac tgt aag aac ggt aaa tta tac cgt tcc aac acc gac act				1167
117 Gly Leu Tyr Cys Lys Asn Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr				
118	270	275	280	
120 aac agt ttg tgt gta gaa ggt caa ggc tct gct caa gct gtt aac aag				1215
121 Asn Ser Leu Cys Val Glu Gly Gln Gly Ser Ala Gln Ala Val Asn Lys				
122	285	290	295	
124 gtc tcc ggc tcc att gct atc tgt ggt acc gat tat cca ggt tct gaa				1263
125 Val Ser Gly Ser Ile Ala Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu				
126	300	305	310	
128 aac atg gtc gtt cct acc gta gtt ggc gct ggt tcc tcc caa cca atc				1311
129 Asn Met Val Val Pro Thr Val Val Gly Ala Gly Ser Ser Gln Pro Ile				

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130 315	320	325	330	
132 aac gtc atc aag gag gac tcc tac tat caa tgg caa ggt aag aag acc				1359
133 Asn Val Ile Lys Glu Asp Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr				
134 335	340	345		
136 tct gcc caa tac tac gtt aac aac gct ggt gtc tct gtg gaa gat ggt				1407
137 Ser Ala Gln Tyr Tyr Val Asn Asn Ala Gly Val Ser Val Glu Asp Gly				
138 350	355	360		
140 tgt atc tgg ggt act gag ggt tcc ggt gtc ggt aac tgg gcc cca gtt				1455
141 Cys Ile Trp Gly Thr Glu Gly Ser Gly Val Gly Asn Trp Ala Pro Val				
142 365	370	375		
144 gtc ttg ggt gct ggt tac act gat ggt atc act tac ttg tcc atc att				1503
145 Val Leu Gly Ala Gly Tyr Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile				
146 380	385	390		
148 cca aac cca aac aaa gaa gca cca aac ttt aac atc aag atc gtt				1551
149 Pro Asn Pro Asn Asn Lys Glu Ala Pro Asn Phe Asn Ile Lys Ile Val				
150 395	400	405	410	
152 gcc acc gat ggc tct acc gtc aat ggt gct tgc tct tac gaa aat ggt				1599
153 Ala Thr Asp Gly Ser Thr Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly				
154 415	420	425		
156 gtc tac tct ggc tct gac ggt tgt act gtt tca gtt act tct				1647
157 Val Tyr Ser Gly Ser Gly Ser Asp Gly Cys Thr Val Ser Val Thr Ser				
158 430	435	440		
160 ggt tct gct aac ttt gtc ttc tac taggcctttt ttcccttgaat attgcaaata				1701
161 Gly Ser Ala Asn Phe Val Phe Tyr				
162 445	450			
164 agcttttgct agtactttttt ttactccgtt cattttatgg tttatttttc aatttagttcg				1761
165 tttttccaca atacaaaaaa acacagtccct ttgtactatc ccttttattt cattattttt				1821
166 tctttttaa gataccacta gatattatca tatatagcat attatataac ataaaaagtc				1881
167 aaaaaaaaaa atgtttttat cacttctat aactgcatac cttttttgc atttcgaatg				1941
168 attgc				1946
170 <210> SEQ ID NO: 2				
171 <211> LENGTH: 450				
172 <212> TYPE: PRT				
173 <213> ORGANISM: Saccharomyces cerevisiae				
175 <220> FEATURE:				
176 <221> NAME/KEY: VARIANT				
177 <222> LOCATION: (1)...(441)				
178 <223> OTHER INFORMATION: Xaa = Any Amino Acid				
180 <400> SEQUENCE: 2				
181 Met Cys Phe Leu Leu Glu Thr Ser Ala Ser Pro Arg Ser Lys Leu Ser				
182 1 5 10 15				
183 Lys Asp Phe Lys Pro Gln Phe Thr Leu Leu Ser Ser Val Thr Lys Lys				
184 20 25 30				
185 Lys Lys Lys Val Arg Pro His Asn Phe Gln Cys Ile His Ser Leu				
186 35 40 45				
187 Asn Phe Val Tyr Phe Leu Phe Ile His Ser Phe Leu Phe Glu Tyr Asn				
188 50 55 60				
189 Gln Leu Leu Val Leu Pro Leu Asn Lys Asn Leu Pro Ser Leu Asn Phe				
190 65 70 75 80				

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191 Ser Arg Asn Ser Ser Met Lys Leu Ser Ala Leu Leu Ala Leu Ser Ala
192 85 90 95
193 Ser Thr Ala Val Leu Ala Ala Pro Ala Val His His Ser Asp Asn His
194 100 105 110
195 His His Asn Asp Lys Arg Ala Val Val Thr Val Thr Gln Tyr Val Asn
196 115 120 125
197 Ala Asp Gly Ala Val Val Ile Pro Ala Ala Thr Thr Ala Thr Ser Ala
198 130 135 140
199 Ala Ala Asp Gly Lys Val Glu Ser Val Ala Ala Ala Thr Thr Thr Leu
200 145 150 155 160
201 Ser Ser Thr Ala Ala Ala Ala Thr Thr Ser Ala Ala Ala Ser Ser Ser
202 165 170 175
203 Ser Ser Ser Ser Ser Ser Ser Ser Ser Val Gly Ser Gly
204 180 185 190
205 Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser Asp Phe Pro Ser Gly Gln
206 195 200 205
207 Gly Ala Val Ser Leu Asp Trp Leu Gly Leu Gly Gly Trp Ala Ser Ile
208 210 215 220
209 Met Asp Met Asn Gly Asn Thr Ala Thr Ser Cys Gln Asp Gly Tyr Tyr
210 225 230 235 240
211 Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala Lys Thr Gln Trp Pro Ser
212 245 250 255
213 Glu Gln Pro Ser Asp Gly Arg Ser Val Gly Gly Leu Tyr Cys Lys Asn
214 260 265 270
215 Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr Asn Ser Leu Cys Val Glu
216 275 280 285
217 Gly Gln Gly Ser Ala Gln Ala Val Asn Lys Val Ser Gly Ser Ile Ala
218 290 295 300
219 Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu Asn Met Val Val Pro Thr
220 305 310 315 320
221 Val Val Gly Ala Gly Ser Ser Gln Pro Ile Asn Val Ile Lys Glu Asp
222 325 330 335
223 Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Val
224 340 345 350
225 Asn Asn Ala Gly Val Ser Val Glu Asp Gly Cys Ile Trp Gly Thr Glu
226 355 360 365
227 Gly Ser Gly Val Gly Asn Trp Ala Pro Val Val Leu Gly Ala Gly Tyr
228 370 375 380
229 Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile Pro Asn Pro Asn Asn Lys
230 385 390 395 400
231 Glu Ala Pro Asn Phe Asn Ile Lys Ile Val Ala Thr Asp Gly Ser Thr
232 405 410 415
233 Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly Val Tyr Ser Gly Ser Gly
234 420 425 430
235 Ser Asp Gly Cys Thr Val Ser Val Thr Ser Gly Ser Ala Asn Phe Val
236 435 440 445
237 Phe Tyr
238 450
241 <210> SEQ ID NO: 3

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Input Set : A:\0050.1491-005.TXT
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242 <211> LENGTH: 3455
243 <212> TYPE: DNA
244 <213> ORGANISM: *Saccharomyces cerevisiae*
246 <220> FEATURE:
247 <221> NAME/KEY: CDS
248 <222> LOCATION: (663)...(3164)
249 <223> OTHER INFORMATION: UTH4
251 <400> SEQUENCE: 3
252 aagctttaac gggatcttc aacaacaaat agcataataa ccaaaaacca gcttcagtgg 60
253 gatcggctta tcgacacgccc ttttttagcg gtctaaacaat ctccgtttat gtcgtatgg 120
254 atttctatac ttgaccctac ttatatttctc gaatatgcct ataaggattt tctcgaaaga 180
255 agggcttcgg gaaagaggcg ctcaggccaa aaatgagccaa aaaaaaaaaa aaaaagaaaa 240
256 gattcgaaga tctatgaaaa atttatgcag attcgttgag agttataagg attttactct 300
257 ttatggttat aggtttcatt ctaaaatcaa gcataaattt tttgtttgtt cttctcttt 360
258 tcctgtcctc ttttttgcc atcctctgtc gccattgaag tcgaaactta tagatagatt 420
259 tactcttgat tctcacccat ctcaggccac ctggacactg tacatggttg tgattgttct 480
260 ctttctcagt tatcgaatt gatcttaggc ttatactccaa aatcggctc tgacacacgccc 540
261 ttatttttgtt ggtttcacct tactaacaca acattctttt attcaatcag atcaataacg 600
262 aaccatttcc atctgccac tcagcatcga tttaactac gtctacatca aataactcct 660
263 ta atg tct tac aat cat cag cct caa cta tct att aac tcc gtc caa 707
264 Met Ser Tyr Asn His Gln Pro Gln Leu Ser Ile Asn Ser Val Gln
265 1 5 10 15
266 Ser Leu Leu Glu Pro Val Thr Pro Pro Leu Gly Gln Met Asn Asn 755
267 tca ctc ttg gag ccc gtg acc cct ccg ctt ttg ggc cag atg aat aac
268 Ser Leu Leu Glu Pro Val Thr Pro Pro Leu Gly Gln Met Asn Asn
269 20 25 30
270 aaa aga aac cat caa aag gct cat tcg ctt gat ctc tct ggt ttt aat 803
271 Lys Arg Asn His Gln Lys Ala His Ser Leu Asp Leu Ser Gly Phe Asn
272 35 40 45
273 cag ttc ata tca tcg aca caa tct ccc ttg gct ttg atg aat aat aca 851
274 Gln Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr
275 50 55 60
276 tca aca tcg aat tct gct aac tct ttt tcc ccg aat cct aat gct gct 899
277 Ser Thr Ser Asn Ser Ala Asn Ser Phe Ser Pro Asn Pro Asn Ala Ala
278 65 70 75
279 agc aac tcc act ggg ctt tca gcc tca atg gca aat cct cca gcc att 947
280 Ser Asn Ser Thr Gly Leu Ser Ala Ser Met Ala Asn Pro Pro Ala Ala
281 80 85 90 95
282 cta cca tta atc aat gag ttt gat ctg gaa atg gat ggt gcc agg aga 995
283 Leu Pro Leu Ile Asn Glu Phe Asp Leu Glu Met Asp Gly Pro Arg Arg
284 100 105 110
285 aaa tca agc cac gat ttc acg gtt gtt gct cct tcg aac tct ggt gtc 1043
286 Lys Ser Ser His Asp Phe Thr Val Val Ala Pro Ser Asn Ser Gly Val
287 115 120 125
288 aat acc tcc agt tta att atg gaa aca cca tcc tct tca gtg act cct 1091
289 Asn Thr Ser Ser Leu Ile Met Glu Thr Pro Ser Ser Val Thr Pro
290 130 135 140
291 gct gca tct ctc aga aat ttt agc aat agt aat aat gct gct tcc aaa 1139
292 Ala Ala Ser Leu Arg Asn Phe Ser Asn Ser Asn Ala Ala Ser Lys
293 145 150 155
294

4/30/01

Please Note :

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/826,752

DATE: 04/30/2001
TIME: 11:04:50

Input Set : A:\0050.1491-005.TXT
Output Set: N:\CRF3\04302001\I826752.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15